

## FIG. 1A

GGATTGAACA AGGACGCATT TCCCCAGTAC ATCCACAAC ATG CTG TCC ACA TCT 54  
Met Leu Ser Thr Ser  
1 5

CGT TCT CGG TTT ATC AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC 102  
Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr  
10 15 20

ACC TTT TTT GAT TAT GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG 150  
Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val  
25 30 35

AAG CAA ATT GGG GCC CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC 198  
Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe  
40 45 50

ATC TTT GGT TTT GTG GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC 246  
Ile Phe Gly Phe Val Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn  
55 60 65

TGC AAA AAG CTG AAG TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC 294  
Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala  
70 75 80 85

ATC TCT GAT CTG CTT TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT 342  
Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser  
90 95 100

GCT GCA AAT GAG TGG GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA 390  
Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr  
105 110 115

GGG CTG TAT CAC ATC GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC 438  
Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu  
120 125 130

CTG ACA ATC GAT AGA TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA 486  
Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu  
135 140 145

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## FIG. 1B

AAA GCC AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG 534  
 Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp  
 150 155 160 165  
 TTG GTG GCT GTG TTT GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC 582  
 Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys  
 170 175 180  
 CAG AAA GAA GAT TCT GTT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA 630  
 Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly  
 185 190 195  
 TGG AAT AAT TTC CAC ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG 678  
 Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu  
 200 205 210  
 CCG CTG CTC ATC ATG GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG 726  
 Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu  
 215 220 225  
 CTT CGG TGT CGA AAC GAG AAG AAG AGG CAT AGG GCA GTG AGA GTC ATC 774  
 Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Val Ile  
 230 235 240 245  
 TTC ACC ATC ATG ATT GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT 822  
 Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile  
 250 255 260  
 GTC ATT CTC CTG AAC ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT 870  
 Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys  
 265 270 275  
 GAA AGC ACC AGT CAA CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT 918  
 Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu  
 280 285 290  
 GGG ATG ACT CAC TGC TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG 966  
 Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly  
 295 300 305

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## FIG. 1C

GAG AAG TTC AGA AGC CTT TTT CAC ATA GCT CTT GGC TGT AGG ATT GCC	1014
Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu Gly Cys Arg Ile Ala	
310 315 320 325	
CCA CTC CAA AAA CCA GTG TGT GGA GGT CCA GGA GTG AGA CCA GGA AAG	1062
Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly Val Arg Pro Gly Lys	
330 335 340	
AAT GTG AAA GTG ACT ACA CAA GGA CTC CTC GAT GGT CGT GGA AAA GGA	1110
Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp Gly Arg Gly Lys Gly	
345 350 355	
AAG TCA ATT GGC AGA GCC CCT GAA GCC AGT CTT CAG GAC AAA GAA GGA	1158
Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu Gln Asp Lys Glu Gly	
360 365 370	
GCC TAGAGACAGA AATGACAGAT CTCTGCTTTG GAAATCACAC GTCTGGCTTC	1121
Ala	
ACAGATGTGT GATTCACAGT GTGAATCTTG GTGTCTACGT TACCAGGCAG GAAGGCTGAG	1271
AGGAGAGAGA CTCCAGCTGG GTTGGAAC AGTATTTTCC AAACCTT CCAGTTCTC	1331
ATTTTTGAAT ACAGGCATAG AGTTCAGACT TTTTTTAAAT AGTAAAAATA AAATTAAAGC	1391
TGAAAACTGC AACTTGTAAG TGTGGTAAAG AGTTAGTTTG AGTTGCTATC ATGTCAAACG	1451
TGAAATGCT GTATTAGTCA CAGAGATAAT TCTAGCTTTG AGCTTAAGAA TTTTGAGCAG	1511
GTGGTATGTT TGGGAGACTG CTGAGTCAAC CCAATAGTTG TTGATTGGCA GGAGTTGGAA	1571
GTGTGTGATC TGTGGGCACA TTAGCCTATG TGCATGCAGC ATCTAAGTAA TGATGTCGTT	1631
TGAATCACAG TATACGCTCC ATCGCTGTCA TCTCAGCTGG ATCTCCATTC TCTCAGGCTT	1691
GCTGCCAAAA GCCTTTTGTG TTTTGTGTTG TATCATTATG AAGTCATGCG TTTAATCACA	1751
TTGAGTGTT TCAGTGCTTC GCAGATGTCC TTGATGCTCA TATTGTTCCC TAATTTGCCA	1811
GTGGGAACTC CTAAATCAAA TTGGCTTCTA ATCAAAGCTT TTAAACCCTA TTGGTAAAGA	1871

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## FIG. 1D

ATGGAAGGTG GAGAAGCTCC CTGAAGTAAG CAAAGACTTT CCTCTTAGTC GAGCCAAGTT 1931  
AAGAATGTTC TTATGTTGCC CAGTGTGTTT CTGATCTGAT GCAAGCAAGA AACACTGGGC 1991  
TTCTAGAACC AGGCAACTTG GGAAGTAGAC TCCAAGCTG GACTATGGCT CTACTTTCAG 2051  
GCCACATGGC TAAAGAAGGT TTCAGAAAGA AGTGGGGACA GAGCAGAACT TTCACCTTCA 2111  
TATATTTGTA TGATCCTAAT GAATGCATAA AATGTTAAGT TGATGGTGAT GAAATGTAAA 2171  
TACTGTTTTT AACAACTATG ATTTGGAAAA TAAATCAATG CTATAACTAT GTTGATAAAA 2231  
G 2232

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# FIG. 2A

CAGGACTGCC TGAGACAAGC CACAAGCTGA ACAGAGAAAG TGGATTGAAC AAGGACGCAT 60  
 TTCCCCAGTA CATCCACAAC ATG <sup>(24)</sup>CTG TCC ACA TCT CGT TCT CGG TTT ATC 110  
 Met Leu Ser Thr Ser Arg Ser Arg Phe Ile  
 1 5 10  
 AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC ACC TTT TTT GAT TAT 158  
 Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr  
 15 20 25  
 GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG AAG CAA ATT GGG GCC 206  
 Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val Lys Gln Ile Gly Ala  
 30 35 40  
 CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC ATC TTT GGT TTT GTG 254  
 Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val  
 45 50 55  
 GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC TGC AAA AAG CTG AAG 302  
 Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys  
 60 65 70  
 TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC ATC TCT GAT CTG CTT 350  
 Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu  
 75 80 85 90  
 TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT GCT GCA AAT GAG TGG 398  
 Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser Ala Ala Asn Glu Trp  
 95 100 105  
 GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA GGG CTG TAT CAC ATC 446  
 Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr Gly Leu Tyr His Ile  
 110 115 120  
 GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGA 494  
 Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg  
 125 130 135  
 TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC 542  
 Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val  
 140 145 150

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## FIG. 2B

ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG TTG GTG GCT GTG TTT 590  
 Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Leu Val Ala Val Phe  
 155 160 165 170

GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC CAG AAA GAA GAT TCT 638  
 Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser  
 175 180 185

GTT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA TGG AAT AAT TTC CAC 686  
 Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly Trp Asn Asn Phe His  
 190 195 200

ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG CCG CTG CTC ATC ATG 734  
 Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu Pro Leu Leu Ile Met  
 205 210 215

GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG CTT CGG TGT CGA AAC 782  
 Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn  
 220 225 230

GAG AAG AAG AGG CAT AGG GCA GTG AGA GTC ATC TTC ACC ATC ATG ATT 830  
 Glu Lys Lys Arg His Arg Ala Val Arg Val Ile Phe Thr Ile Met Ile  
 235 240 245 250

GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT GTC ATT CTC CTG AAC 878  
 Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn  
 255 260 265

ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT GAA AGC ACC AGT CAA 926  
 Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln  
 270 275 280

CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT GGG ATG ACT CAC TGC 974  
 Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu Gly Met Thr His Cys  
 285 290 295

TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG GAG AAG TTC AGA AGG 1022  
 Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe Arg Arg  
 300 305 310

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## FIG. 2C

TAT CTC TCG GTG TTC TTC CGA AAG CAC ATC ACC AAG CGC TTC TGC AAA 1070  
 Tyr Leu Ser Val Phe Phe Arg Lys His Ile Thr Lys Arg Phe Cys Lys  
 315 320 325 330

CAA TGT CCA GTT TTC TAC AGG GAG ACA GTG GAT GGA GTG ACT TCA ACA 1118  
 Gln Cys Pro Val Phe Tyr Arg Glu Thr Val Asp Gly Val Thr Ser Thr  
 335 340 345

AAC ACG CCT TCC ACT GGG GAG CAG GAA GTC TCG GCT GGT TTA 1160  
 Asn Thr Pro Ser Thr Gly Glu Gln Glu Val Ser Ala Gly Leu  
 350 355 360

TAAAACGAGG AGCAGTTTGA TTGTTGTTTA TAAAGGGAGA TAACAATCTG TATATAACAA 1220  
 CAAACTTCAA GGGTTTGTG AACAATAGAA ACCTGTAAAG CAGGTGCCCA GGAACCTCAG 1280  
 GGCTGTGTGT ACTAATACAG ACTATGTCAC CCAATGCATA TCCAACATGT GCTCAGGGAA 1340  
 TAATCCAGAA AACTGTGGG TAGAGACTTT GACTCTCCAG AAAGCTCATC TCAGCTCCTG 1400  
 AAAAATGCCT CATTACCTTG TGCTAATCCT CTTTTTCTAG TCTTCATAAT TTCTTCACTC 1460  
 AATCTCTGAT TCTGTCAATG TCTTGAAATC AAGGGCCAGC TGGAGGTGAA GAAGAGAATG 1520  
 TGACAGGCAC AGATGAATGG GAGTGAGGGA TAGTGGGGTC AGGGCTGAGA GGAGAAGGAG 1580  
 GGAGACATGA GCATGGCTGA GCCTGGACAA AGACAAAGGT GAGCAAAGGG CTCACGCATT 1640  
 CAGCCAGGAG ATGATACTGG TCCTTAGCCC CATCTGCCAC GTGTATTTAA CCTTGAAGGG 1700  
 TTCACCAGGT CAGGGAGAGT TTGGGAACTG CAATAACCTG GGAGTTTTTG TGGAGTCCGA 1760  
 TGATTCTCTT TTGCATAAGT GCATGACATA TTTTGTCTT ATTACAGTTT ATCTATGGCA 1820  
 CCCATGCACC TTACATTGGA AATCTATGAA ATATCATGCT CCATTGTTCA GATGCTTCTT 1880  
 AGGCCACATC CCCCTGTCTA AAAATTCAGA AAATTTTGT TTATAAAAGA TGCATTATCT 1940  
 ATGATATGCT AATATATGTA TATGCAATAT AAAATTTAG 1979

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FIG. 3(A)

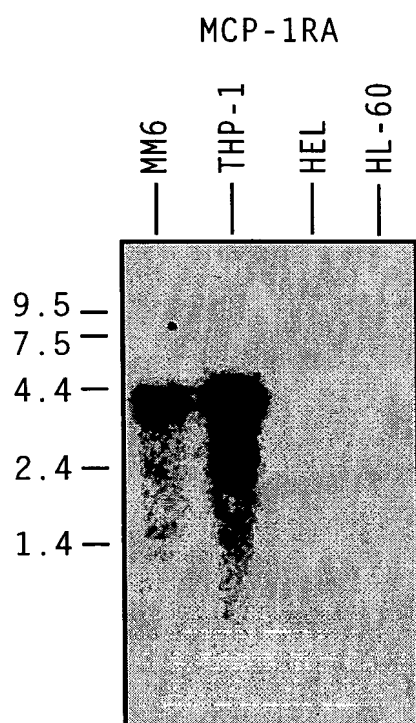


FIG. 3(B)

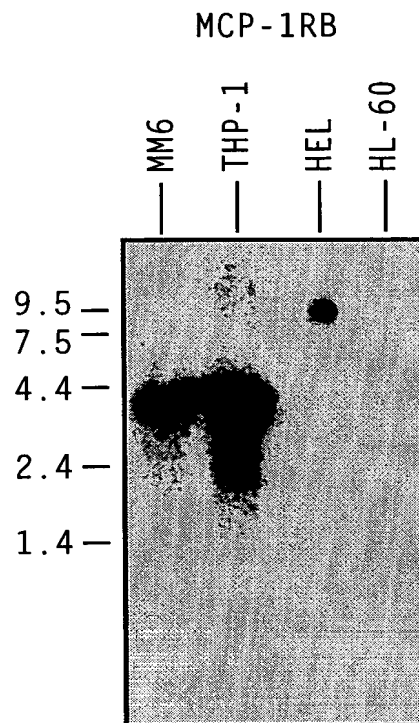




FIG.4(A)

MCP-1RA (CCR2-A)	MLSTSRSRFIRNTNESGEEVTTFDDYDYG--APCHKFDVKQIGAQLLPPL	48
MIP-1 $\alpha$ /RANTESR	M-----ETPNTTEDYDITTEFDYGDATPCQKVNERAFGAQLLPPL	40
HUMSTR	MEGIS----IYTSNYTEEMGS-GDYDSMK-EPCFREANANFNKIFLPTI	44
IL-8RA	MSNITDPQ-MWDFDDLNTGMPPADEDY---SPC-MLETETLNKYVVIIA	45
IL-8RB	MESDSFEDFWKGEDLSNYSYSTLPFPFLDAAPC-EPESEINKYFVVII	49
	48 1 69 79 2	
MCP-1RA (CCR2-A)	YSLVFIIFGFVGNMLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLW	98
MIP-1 $\alpha$ /RANTESR	YSLVFVIGLVGNILVVLVLVQYKRLKNMTSIYLLNLAISDLLFLITLPLW	90
HUMSTR	YSIIIFLTGIVGNGLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPLW	94
IL-8RA	YALVFLLSLLGNSLVMLVILYSRVGRSVTDVYLLNLALADLLFALTLPW	95
IL-8RB	YALVFLLSLLGNSLVMLVILYSRVGRSVTDVYLLNLALADLLFALTLPW	99
	101 115 3 136	
MCP-1RA (CCR2-A)	AH-SAAEWEVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVHAVF	147
MIP-1 $\alpha$ /RANTESR	IDYKLKDDWVFGDAMCKILSGFYTYGLYSEIFFIILLTIDRYLAIVHAVF	140
HUMSTR	AV-DAVANWYFGNLFCKAVHVIYTVNLYSSVLILAFISLDYLAIVHATN	143
IL-8RA	AA-SKVGWIFGTFLCKVVSLLKEVNFYSGILLACISVDYLAIVHATR	144
IL-8RB	AA-SKVGWIFGTFLCKVVSLLKEVNFYSGILLACISVDYLAIVHATR	148
	154 4 178	
MCP-1RA (CCR2-A)	ALKARTVTFGVMTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFP--	195
MIP-1 $\alpha$ /RANTESR	ALRARTVTFGVITSIIIALAILASMPGLYFSKTQWEFTHTCSLHFPHE	190
HUMSTR	SQRPRKLLAEKVYVGVWIPALLTIPDFIFANVSEADRYICDRFYPN-	192
IL-8RA	TLTQKR-HLVKFVCLGCWGLSMNLSLPFFLFRQAYHPNNSPVCYEV LGN	193
IL-8RB	TLTQKRYLVKFI-CLSIWGLSLLLALPVLLFRRTVYSSNVSPACYEDMGN	197
	204 5 231	
MCP-1RA (CCR2-A)	--RGWNNFHTIMRNILGLVLP LLIMVICYS GILKTLLRCRNEKKRHRVR	243
MIP-1 $\alpha$ /RANTESR	SLREWKL FQALKNL FGLVLP LLIMVICYTGIIKILLRRPNEKKS-KAVR	239
HUMSTR	--DLWVVVFQFHIMVGLILPGIVILFCYCIISKLSHSGHQKR-KALK	239
IL-8RA	DTAKWRMVLRI LPHTFGFIVPLFVMLFCYGFTLRTL FKAHMGQK-HRAMR	242
IL-8RB	NTANWRMLLRIL PQSFGFIVPLLIMLFCYGFTLRTL FKAHMGQ-KHRAMR	246
	244 6 268	
MCP-1RA (CCR2-A)	VIFTIMIVYFLFWTPYNIIVILLNTFQEF-FGLSNCESTSQLDQATQVTET	292
MIP-1 $\alpha$ /RANTESR	LIFVIMIIFFLFWTPYNLTILISVFQDF-LFTHCEQSRHLDLAVQVTEV	288
HUMSTR	TTVILILAFFACWLPYYIGISIDSFILLEIKQGEFENTVHKWISITEA	289
IL-8RA	VIFAVVLIFLLCWL PYNLVLLADTLMRTQVIQETCERRNIGRALDATEI	292
IL-8RB	VIFAVVLIFLLCWL PYNLVLLADTLMRTQVIQETCERRNHIDRALDATEI	296

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FIG. 4(B)

	295	7	313	
MCP-1RA (CCR2-A)	LGMTHCCINPIIYAFVGEKFRSL*	FHIALGCRIAPLQKPVC	GGPGVVRPGKN	342
MIP-1 $\alpha$ /RANTESR	IAYTHCCVNPVIYAFVGERFRKYL	RQLFHRVA-----	VHLVKW	327
HUMSTR	LAFHCCLNPIIYAFVGERFKTS	AQHALTS-----	VSRGSS	325
IL-8RA	LGFLHSCLNPIIYAFVGERHGF	LKILA-----	MHGLVS	327
IL-8RB	LGILHSCLNPLIYAFVGERHGL	LKILAIH-----	GLIS	331
MCP-1RA (CCR2-A)	VKVTTQGLLDGRGKGKSI	GRAPEASLQDKEGA		374
MIP-1 $\alpha$ /RANTESR	LPFLSVDRLE-RVSSTS-	PSTGEHEL--SAGF		355
HUMSTR	LKILSKGK---RGHSSV	STESESS--FHSS		352
IL-8RA	KEFLARH---RVTSYT-	SSSVNVS----SNL		350
IL-8RB	KDSLPKDS---RPSFVG-	SSSGHTS----TTL		355

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FIG. 5

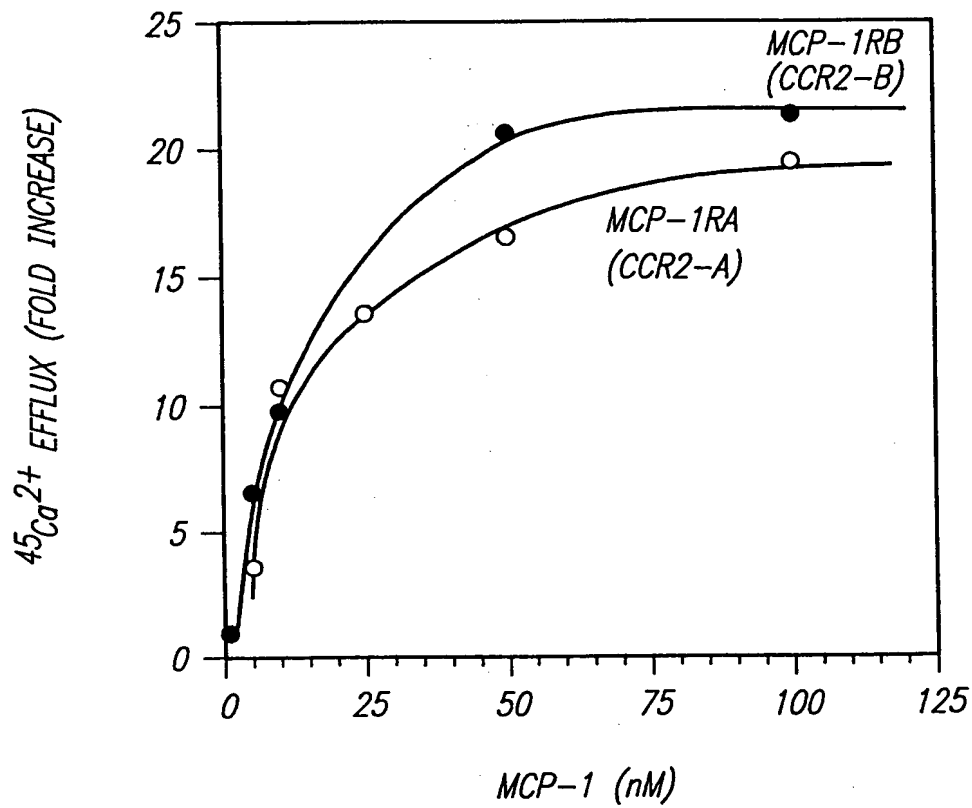
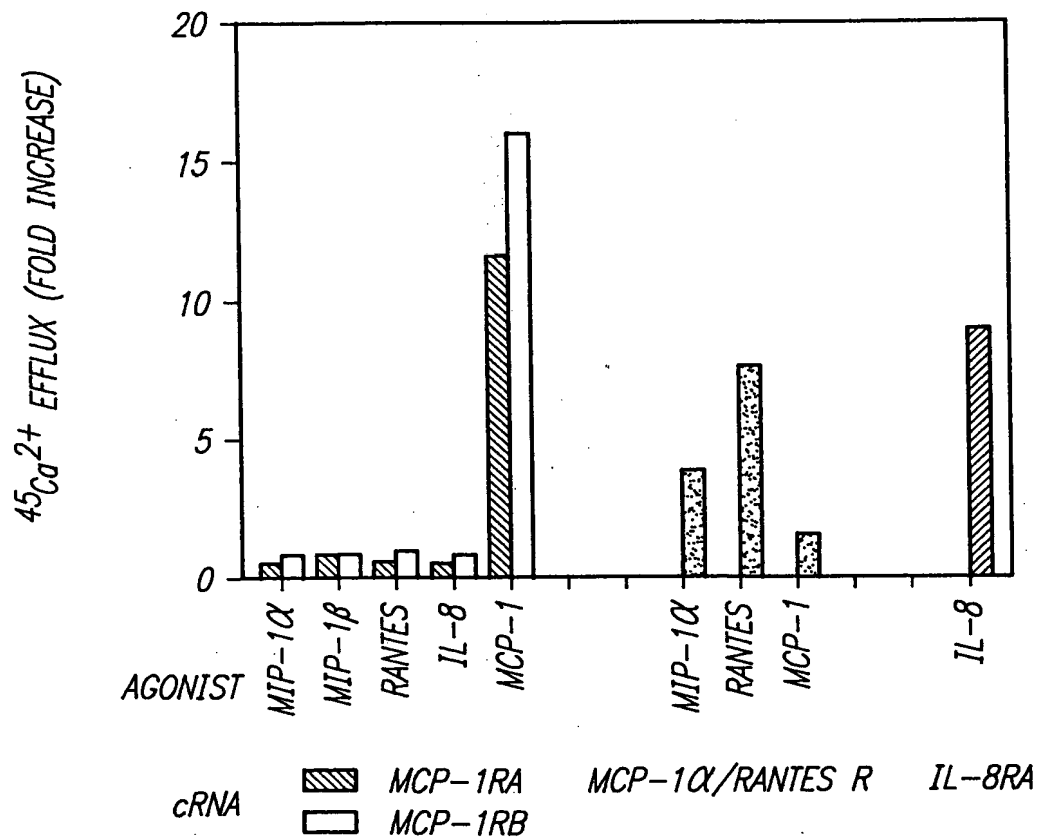


FIG. 6



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FIG. 7A MCP-1RB

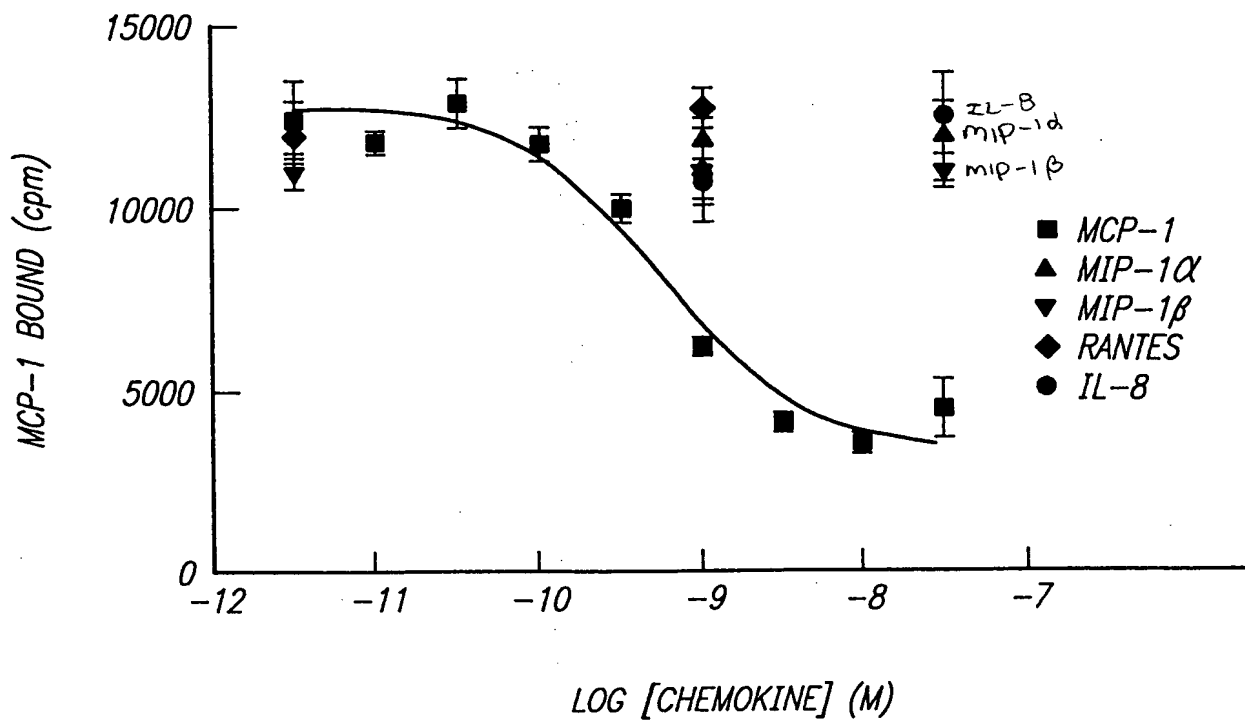
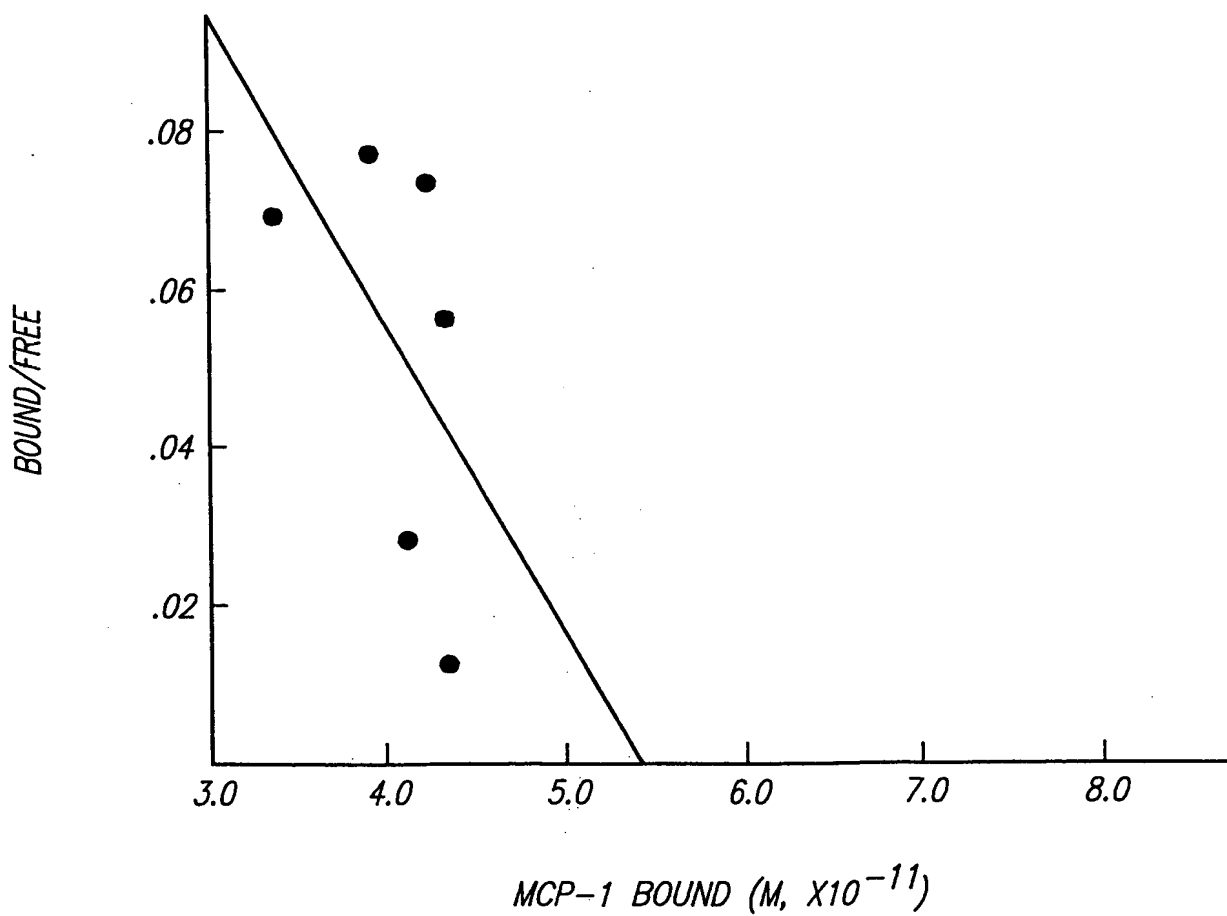
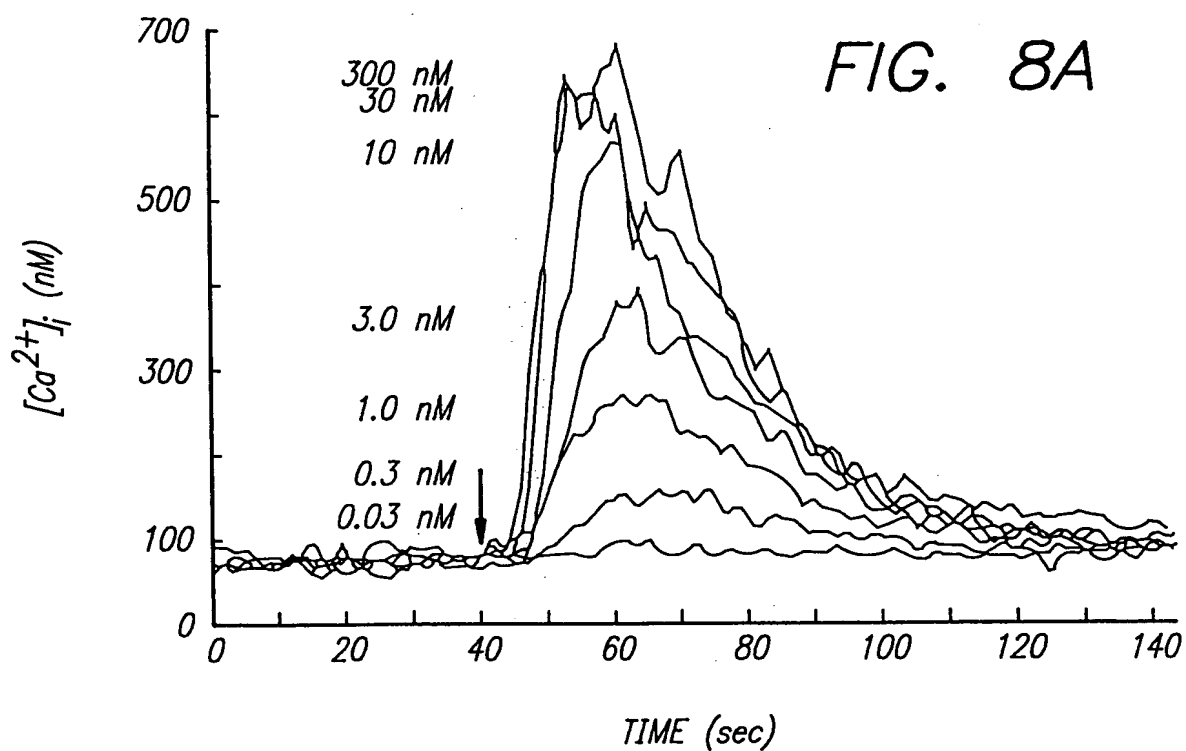
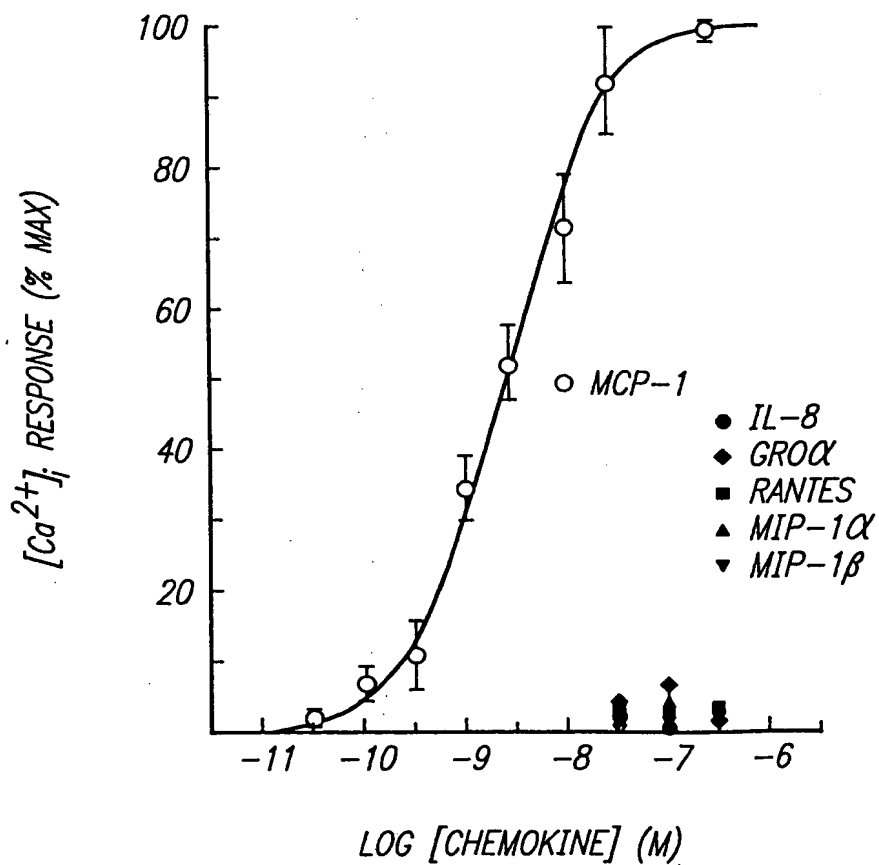


FIG. 7B



**FIG. 8B**

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FIG. 8C

